AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Currently amended) A genotyping method comprising

using hybridizing a target nucleic acid to a DNA chip on which an optimal probe pair is immobilized,

wherein the optimal probe pair consists of a wild type-perfect match probe for a mutation site on the target nucleic acid and a mutant type-perfect match probe are immobilized for each the mutation site,-

wherein the optimal probe pair is selected by:

designing a plurality of probe pairs for the mutation site, wherein a probe pair consists of a wild type-perfect match probe and a mutant type-perfect match probe;

immobilizing the plurality of probe pairs on a substrate to manufacture an optimal probe pair screening chip;

hybridizing a standard nucleic acid to the optimal probe pair screening chip;

collecting quantitative hybridization intensity data;

calculating a value for each probe pair of the following equation:

$$\{Mean(\ln(r^{wt})) - 2\ SD(\ln(r^{wt}))/\sqrt{N^{wt}}\} - \{Mean(\ln(r^{mt})) + 2SD(\ln(r^{mt}))/\sqrt{N^{mt}}\}$$

wherein N denotes a number of times hybridization of the standard nucleic acid has been performed;

r^{wt} is a ratio between a hybridization intensity of a wild type standard nucleic acid to the wild type-perfect match probe and a hybridization intensity of the wild type standard nucleic acid to the mutant type-perfect match probe;

r^{mt} is a ratio between a hybridization intensity of a mutant type standard nucleic acid to the wild type-perfect match probe and a hybridization intensity of the mutant type standard nucleic acid to the mutant type-perfect match probe; and

$Mean$ and SD denote a mean value and a standard deviation, respectively, of N ln(r) values, which are obtained by hybridizing the standard nucleic acid to the DNA chip N times; and

selecting the probe pair having the largest value as the optimal probe pair.

2. (Currently amended) The genotyping method of claim 1, wherein at least two optimal probe pairs ~~for the mutation site~~ are immobilized ~~for each mutation site of~~ on the DNA chip.

3. (Currently amended) The genotyping method of claim 2, wherein at least two wild type-perfect match probes <u>for the mutation site</u> are arranged side by side and at least two mutant type-perfect match probes <u>for the mutation site</u> are arranged side by side adjacent to the wild type-perfect match probes ~~for each mutation site of~~<u>on</u> the DNA chip.

4. (<u>Cancelled</u>)

5. (Currently amended) The genotyping method of claim 1, <u>further</u> comprising:

(a) setting up a genotyping algorithm ~~using data obtained from~~<u>for</u> hybridization of ~~an identified~~ <u>a</u> standard nucleic acid to the DNA chip; and

(b) genotyping ~~an unknown~~<u>the</u> target nucleic acid by substituting an input vector that ~~are~~ <u>is</u> calculated from hybridization of the target nucleic acid to the DNA chip into the genotyping algorithm.

6. (Currently amended) The genotyping method of claim 5, wherein (a) comprises:

(a-1) collecting quantitative hybridization intensity data obtained from hybridization of the ~~identified~~ standard nucleic acid to the DNA chip;

(a-2) calculating ~~the~~ a ratio, r_{ij}, for every pairing of a wild type-perfect match probe (wp_i) of an optimal probe pair (*i*) immobilized on the DNA chip for the mutation site on the target nucleic acid and a mutant type-perfect match probe (mp_j) of an optimal probe pair (*j*) immobilized on the DNA chip for the mutation site on the target nucleic acid,

wherein the ratio, r_{ij}, is between ~~the~~ a hybridization intensity of the standard nucleic acid to the wild type-perfect match probe (wp_i) and ~~the~~ a hybridization intensity of the standard nucleic acid to the mutant type-perfect match probe (mp_j) ~~for every probe pair~~,

selecting ~~the~~ a Hodge-Lehman median from among the calculated ratios ~~using Hodge-lehman estimation~~, and

taking the ~~natural~~ logarithm of the median as a ratio component of a vector ~~used to set up the genotyping algorithm~~ for the DNA chip; and

(a-3) repeating (a-1) and (a-2) with a plurality of DNA chips to obtain ratio components for a set of vectors ~~and setting up the genotyping algorithm using the set of vectors~~.

7. (Currently amended) The genotyping method of claim 6, wherein (a-3) further comprises calculating logistic regression coefficients for ~~the genotyping algorithm using~~ the set of vectors.

8. (Currently Amended) The genotyping method of claim 6, wherein (a-2) further comprises

obtaining a product, a_{ij}, for every pairing of a wild type-perfect match probe (wp_i) of an optimal probe pair (i) immobilized on the DNA chip for the mutation site on the target nucleic acid and a mutant type-perfect match probe (mp_j) of an optimal probe pair (j) immobilized on the DNA chip for the mutation site on the target nucleic acid,

wherein the product, a_{ij}, is obtained by multiplying the hybridization ~~intensities~~ intensity of ~~each probe pair~~ the standard nucleic acid to the wild type-perfect match probe (wp_i)' and the hybridization intensity of the standard nucleic acid to the mutant type-perfect match probe (mp_j),

selecting the Hodge-Lehman median from among the products ~~using Hodge-lehman estimation~~,

dividing the ~~natural~~ logarithm of the median by two to obtain an intensity component of the vector for the DNA chip ~~used to set up the genotyping algorithm~~;

wherein the genotyping method further comprises

plotting a graph with the Y-axis parameterized by the ratio component and the X-axis parameterized by the intensity component before (a-3); and

the genotyping algorithm comprises logistic regression coefficients ~~is set up in (a-3) using~~ of all of the ratio components if the ratio components ~~of the graph has a independence on~~ are independent of the intensity components or comprises logistic regression coefficients ~~using~~ of only ~~some~~ the ratio components which are independent of the intensity components if the ratio components ~~of the graph has a dependence~~ are dependent on the intensity components.

9. (Currently Amended) The genotyping method of claim 6, wherein (a-2) further comprises

~~taking the larger of~~comparing, for every pairing of a wild type-perfect match probe (wp$_i$) of an optimal probe pair (*i*) immobilized on the DNA chip for the mutation site on the target nucleic acid and a mutant type-perfect match probe (mp$_j$) of an optimal probe pair (*j*) immobilized on the DNA chip for the mutation site on the target nucleic acid, the hybridization ~~intensities~~ intensity of ~~each probe pair~~the standard nucleic acid to the wild type-perfect match probe (wp$_i$) and the hybridization intensity of the standard nucleic acid to the mutant type-perfect match probe (mp$_j$), to determine which is the larger,

selecting the Hodge-Lehman median from among the ~~selected~~ larger hybridization intensities ~~using Hodge-lehman estimation,~~

taking the ~~natural~~ logarithm of the median as an intensity component of ~~a~~ the vector ~~for the DNA chip~~used to set up the genotyping algorithm;

the genotyping method further comprises

plotting a graph with the Y-axis parameterized by the ratio component and the X-axis parameterized by the intensity component before (a-3); and

the genotyping algorithm comprises logistic regression coefficients of ~~is set up in (a-3)~~ ~~using~~ all of the ratio components if the ratio component**s** ~~of the graph has a independence on~~are independent of the intensity component**s** or comprises logistic regression coefficients of ~~using~~ only ~~some~~ the ratio components which are independent of the intensity component**s** if the ratio components ~~of the graph has a dependence~~are dependent on the intensity component**s**.

10. (Currently amended) The genotyping method of claim 6, further comprising

filtering ~~out~~ quantitative hybridization intensity data obtained from bad spots from the quantitative hybridization intensity data collected in step (a-1) before (a-2),

wherein a bad spot on the DNA chip ~~that have~~has a larger diameter than an effective spot diameter ~~from the quantitative hybridization intensity data collected in step (a-1) before (a-2)~~.

11. (Currently amended) The genotyping method of claim 5, wherein (b) comprises:

(b-1) collecting quantitative hybridization data obtained from hybridization of the ~~unknown~~ target nucleic acid to the DNA chip;

(b-2) calculating ~~the~~ a ratio, r_{ij}, for every pairing of a wild type-perfect match probe (wp_i) of an optimal probe pair (i) immobilized on the DNA chip for the mutation site on the target nucleic acid and a mutant type-perfect match probe (mp_j) of an optimal probe pair (j) immobilized on the DNA chip for the mutation site on the target nucleic acid,

wherein the ratio, r_{ij}, is between ~~the~~ a hybridization intensity of the target nucleic acid to the wild type-perfect match probe (wp_i) and ~~the~~ a hybridization intensity of the target nucleic acid to the mutant type-perfect match probe (mp_j) ~~for every probe pair~~,

selecting the Hodge-Lehman median from among the calculated ratios ~~using Hodge-lehman estimation~~, and

taking the ~~natural~~ logarithm of the median as an input vector for genotyping; and

(b-3) substituting the input vector into the genotyping algorithm to genotype the target nucleic acid.

12. (Currently Amended) The genotyping method of claim 11, wherein (b-3) comprises

calculating ~~the~~ a posterior ~~probabilities~~ probability that the target nucleic acid is a wild type and a posterior probability that the target nucleic acid is ~~or~~ a mutant type by substituting the input vector into the genotyping algorithm and

determining the genotype of the target nucleic acid to be a wild type if the posterior probability that the target nucleic acid is a wild type is greater than the posterior probability that the target nucleic acid is a mutant type or determining the genotype of the target nucleic acid to be a mutant type if the posterior probability that the target nucleic acid is a wild type is less than the posterior probability that the target nucleic acid is a mutant ~~depending on the greater posterior probability~~.

13. (Currently Amended) The genotyping method of claim ~~11~~12, wherein (b-3) <u>further</u> comprises:

~~calculating the posterior probabilities that the target nucleic acid is wild-type or a mutant type by substituting the input vector into the genotyping algorithm to determine the genotype of the target nucleic acid to be a wild-type or a mutant type depending on the greater posterior probability; and~~

validating <u>the genotype determination based on a reliability requirement, wherein</u> the reliability <u>requirement is that</u>~~of~~ the ~~greater~~ posterior probability <u>of the determined genotype be</u> at a predetermined significance level and

deferring ~~genotyping~~<u>determination of a genotype</u> of the target nucleic acid if the reliability requirement is not satisfied.

14. (Currently Amended) The genotyping method of claim 11, further comprising

filtering ~~out~~ quantitative hybridization intensity data obtained from bad spots <u>from the quantitative hybridization intensity data collected in step (b-1) before (b-3),</u>

<u>wherein a bad spot on the DNA chip has</u>~~that have~~ a larger diameter than an effective spot diameter ~~from the quantitative hybridization intensity data collected in step (b-1) before (b-3)~~.

15. (Currently Amended) The genotyping method of claim 5, further comprising

correcting the genotyped results from step (b) ~~based on cross-hybridization data of the probe pair for each mutation site~~.

16. (Withdrawn) A DNA chip used for a genotyping method, comprising an optimal probe pair of a wild type-perfect match probe and a mutant type-perfect match probe which are immobilized for each mutation site.